## AMENDMENTS TO THE CLAIMS:

The listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): A method of domain specific gene evolution of a target nucleic acid encoding ~~an amino acid~~ a polypeptide sequence of interest, said method comprising:

contacting ~~a~~ the target nucleic acid with a recombinase and a first plurality of pairs of single-stranded-targeting polynucleotides which are substantially complementary to each other, wherein each said targeting polynucleotide comprises a homology clamp that substantially corresponds to or is substantially complementary to a first predetermined sequence of said target nucleic acid encoding a first domain of a polypeptide, said first plurality of pairs comprising a first library of nucleic acids having mismatches between said targeting polynucleotides and said first predetermined sequence, to form a first library of altered target nucleic acids;

and repeating said contacting on said library of altered nucleic acids whereby said first predetermined sequence undergoes domain specific gene evolution.

Claim 2 (currently amended): A method according to claim 1, further comprising:

contacting said target nucleic acid or said first library of altered target nucleic acids with a second plurality of pairs of single-stranded targeting polynucleotides which are substantially complementary to each other and are not substantially complementary to said first plurality of polynucleotides, wherein each said targeting polynucleotide comprises a homology clamp that substantially corresponds to or is substantially complementary to a second predetermined sequence of said target nucleic acid encoding a second domain of said polypeptide, said second plurality of pairs comprising a second library of nucleic acids having mismatches between said second targeting polynucleotides and said second predetermined sequence, to form a second library of altered target nucleic acids whereby said second predetermined sequence undergoes domain specific gene evolution.

Claim 3 (currently amended): A method of domain specific gene evolution comprising:

a) contacting a target nucleic acid encoding a polypeptide of interest with a recombinase and a first pair of single stranded-targeting polynucleotides which are substantially

complementary to each other, wherein each said targeting polynucleotide comprises a homology clamp that substantially corresponds to or is substantially complementary to a first predetermined sequence of said nucleic acid encoding a first domain of said polypeptide to form a first recombination intermediate;

b) contacting said recombination intermediate with a single strand-specific nuclease to form a nicked ~~or open-ended~~ target nucleic acid; and

c) reassembling and recombining said nicked or ~~open-ended~~ target nucleic acid to evolve a first library of altered target nucleic acids whereby said first predetermined sequence undergoes domain specific gene evolution.

Claim 4 (currently amended): A method according to claim 3 further comprising:

d) ~~combining~~ contacting said target nucleic acid or said first library of altered target nucleic acids with a second pair of single-stranded targeting polynucleotides which are substantially complementary to each other and are not substantially complementary to said first pair of polynucleotides, wherein each targeting polynucleotide comprises a homology clamp that substantially corresponds to or is substantially complementary to a second predetermined sequence of said target nucleic acid encoding a second domain of said polypeptide, to form a second recombination intermediate, wherein said contacting of step b) is of said second recombination intermediate with said nuclease.

Claim 5 (cancelled)

Claim 6 (cancelled)

Claim 7 (previously amended)

Claim 8 (currently amended) A method according to claim 7 further comprising:

c) ~~adding to~~ contacting said chromosomal nucleic acid or said first library of altered target nucleic acids a second plurality of pairs of single-stranded targeting polynucleotides which are substantially complementary to each other and are not substantially complementary to said first plurality of polynucleotides, wherein each said polynucleotide comprises a homology clamp that substantially corresponds to or is substantially complementary to a second preselected sequence of said target nucleic acid, said second plurality of pairs comprising a second library of nucleic acids having mismatches between said targeting polynucleotides and said second preselected

sequence, to evolve a second library of altered target nucleic acids, wherein said repeating is on said second library of altered target nucleic acids.

Claim 9 (cancelled)

Claim 10 (currently amended): A method according to any one of claims 1, 2, 3, 4, ~~5, 6,~~ 7, 8, 25, 26, ~~27,~~ and 28 further comprising introducing <u>the resultant product</u> ~~said library of altered target nucleic acids~~ into cells to form a cellular library comprising variant nucleic acid sequences.

Claim 11 (currently amended): A method according to claim 10 further comprising expressing said <u>cellular</u> library of altered target nucleic acids to generate a library of variant polypeptides.

Claim 12 (previously amended)

Claim 13 (previously amended)

Claim 14 (currently amended): A method according to claim 11 further comprising secreting said <u>cellular</u> library of variant ~~amino acid sequences~~ <u>polypeptides</u>.

Claim 15 (previously amended)

Claim 16 (previously amended)

Claim 17 (previously amended)

Claim 18 (currently amended): A method according to claim 1, 2, 3, 4, ~~5, 6,~~ 7, 8, 25, 26, ~~27,~~ or 28 wherein said targeting polynucleotides are coated with said recombinase.

Claim 19 (currently amended): A method according to claim 1, 2, 3, 4, ~~5, 6,~~ 7, 8, 25, 26, ~~27,~~ or 28 wherein said recombinase is a species of prokaryotic recombinase.

Claim 20 (currently amended): A method according to claim 1, 2, 3, 4, ~~5, 6,~~ 7, 8, 25, 26, ~~27,~~ or 28 wherein said recombinase is a species of eukaryotic recombinase.

Claim 21 (previously amended)

Claim 22 (currently amended):  A method according to claim 1, 2, 3, 4, 5, 6, 7, 8, 25, 26, 27, or 28 wherein at least one of said targeting polynucleotides further comprises a chemical substituent.

Claim 23 (currently amended):  A method according to claim 1, 2, 3, 4, 5, 6, 7, 8, 25, 26, 27, or 28 wherein said target amino nucleic acid comprises a complementary complementarity determining region

Claim 24 (currently amended):  A method according to claim 1, 2, 3, 4, 5, 6, 7, 8, 25, 26, 27, or 28 wherein said target nucleic acid comprises an expression vector.

Claim 25 (previously added)

Claim 26 (previously added)

Claim 27 (previously added)

Claim 28 (previously added)

Claim 29 (currently amended):  A method according to claim 1, 2, 3, 4, 5, 6, 7, 8, 25, or 26, 27, or 28 further comprising contacting said recombination intermediate with a recombination proficient cell.